



Genetic diversity of *Lagerstroemia* (Lythraceae) species assessed by simple sequence repeat markers

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ABSTRACT. *Lagerstroemia* (crape myrtle) are famous ornamental plants with large pyramidal racemes, long flower duration, and diverse colors. However, little is known about the genetic structure and diversity of germplasm in *Lagerstroemia*. We genotyped 81 *L. indica* cultivars, five other species of *Lagerstroemia*, and 10 interspecific hybrids using 30 simple sequence repeat markers; 275 alleles were generated with a mean of nine alleles per locus. The mean polymorphism information content value, a measure of gene diversity, was 0.63, with a range from 0.25 to 0.86. The mean observed heterozygosity (0.51) tended to be lower than the mean expected heterozygosity (0.67). The mean F-statistics (F_{ST} , F_{IS} , and F_{IT}) were 0.05, 0.20, and 0.24, respectively, indicating a high level of genetic variation among cultivars. Clustering analysis based on genetic distance divided the 96 genotypes into three distinct groups, which corresponded with their genetic backgrounds and geographic regions. *L. indica* cultivars and the other five *L. species* were grouped into different sub-clusters. Chinese and North American cultivars were divided into different clusters. These data about the genetic relationship among cultivars demonstrated the potential value of *L. indica* cultivars and

other *Lagerstroemia* species for widening the genetic basis of breeding programs for this ornamental flower.

Key words: *Lagerstroemia*; SSR; Genetic diversity; Cluster analysis